

51791AUSD1.ST25  
SEQUENCE LISTING

<110> Harkins, Richard  
Parkes, Deborah  
Parry, Gordon  
Schneider, Douglas  
Steinbrecher, Renate

<120> DNA Encoding a Novel RG-1 Polypeptide

<130> 51791AUSD1

<150> US 60/172,370  
<151> 1999-12-16

<150> US 09/732,357  
<151> 2000-12-07

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<170> PatentIn version 3.1

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tctcccacgt cctatctgcc tctcgctgga ggccaggccg tgccatcg aagacaggag 180  
gaactggagc ctcattggcc ggccgggggc gcccgcctcg ggctaaata ggagctccgg 240  
gctctggctg ggacccgacc gtcggccgc gtcggccgc tgctcctgcc gggtg atg 298  
Met  
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gaa aac ccc agc ccc gcc gcc gcc ctg ggc aag gcc ctc tgc gct ctc 346  
Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys Ala Leu  
5 10 15  
ctc ctg gcc act ctc ggc gcc gcc ggc cag cct ctt ggg gga gag tcc 394  
Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly Gly Glu Ser  
20 25 30  
atc tgt tcc gcc gga gcc ccg gcc aaa tac agc atc acc ttc acg ggc 442  
Ile Cys Ser Ala Gly Ala Pro Ala Lys Tyr Ser Ile Thr Phe Thr Gly  
35 40 45  
aag tgg agc cag acg gcc ttc ccc aag cag tac ccc ctg ttc cgc ccc 490

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Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr Pro Leu Phe Arg Pro	50	55	60	65	
cct gcg cag tgg tct tcg ctg ggg gcc gcg cat agc tcc gac tac	70	75	80		538
Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala Ala His Ser Ser Asp Tyr					
agc atg tgg agg aag aac cag tac gtc agt aac ggg ctg cgc gac ttt	85	90	95		586
Ser Met Trp Arg Lys Asn Gln Tyr Val Ser Asn Gly Leu Arg Asp Phe					
gcg gag cgc ggc gag gcc tgg gcg ctg atg aag gag atc gag gcg gcg	100	105	110		634
Ala Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala Ala					
ggg gag gcg ctg cag agc gtg cac gcg gtg ttt tcg gcg ccc gcc gtc	115	120	125		682
Gly Glu Ala Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala Val					
ccc agc ggc acc ggg cag acg tcg gcg gag ctg gag gtg cag cgc agg	130	135	140	145	730
Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val Gln Arg Arg					
cac tcg ctg gtc tcg ttt gtg gtg cgc atc gtg ccc agc ccc gac tgg	150	155	160		778
His Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp Trp					
ttc gtg ggc gtg gac agc ctg gac ctg tgc gac ggg gac cgt tgg cgg	165	170	175		826
Phe Val Gly Val Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp Arg					
gaa cag gcg gcg ctg gac ctg tac ccc tac gac gcc ggg acg gac agc	180	185	190		874
Glu Gln Ala Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp Ser					
ggc ttc acc ttc tcc ccc aac ttc gcc acc atc ccg cag gac acg	195	200	205		922
Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr					
gtg acc gag ata acg tcc tcc tct ccc agc cac ccg gcc aac tcc ttc	210	215	220	225	970
Val Thr Glu Ile Thr Ser Ser Pro Ser His Pro Ala Asn Ser Phe					
tac tac cca cgg ctg aag gcc ctg cct ccc atc gcc agg gtg aca ctg	230	235	240		1018
Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr Leu					
gtg cgg ctg cga cag agc ccc agg gcc ttc atc cct ccc gcc cca gtc	245	250	255		1066
Val Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala Pro Val					
ctg ccc agc agg gac aat gag att gta gac agc gcc tca gtt cca gaa	260	265	270		1114
Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser Val Pro Glu					
acg ccg ctg gac tgc gag gtc tcc ctg tgg tcg tcc tgg gga ctg tgc	275	280	285		1162
Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu Cys					

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gga ggc cac tgt ggg agg ctc ggg acc aag agc agg act cgc tac gtc	1210
Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser Arg Thr Arg Tyr Val	
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cgg gtc cag ccc gcc aac aac ggg agc ccc tgc ccc gag ctc gaa gaa	1258
Arg Val Gln Pro Ala Asn Asn Gly Ser Pro Cys Pro Glu Leu Glu Glu	
310 315 320	
gag gct gag tgc gtc cct gat aac tgc gtc taa gaccagagcc ccgcagcccc	1311
Glu Ala Glu Cys Val Pro Asp Asn Cys Val	
325 330	
tggggccccc cggagccatg ggggtgtcggg ggctcctgtg caggctcatg ctgcaggcgg	1371
ccgagggcac agggggtttc gcgctgctcc tgaccgcgtt gaggccgcgc cgaccatctc	1431
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Ser Ile Cys Ser Ala Gly Ala Pro Ala Lys Tyr Ser Ile Thr Phe Thr  
 35 40 45

Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr Pro Leu Phe Arg  
 50 55 60

Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala Ala His Ser Ser Asp  
 65 70 75 80

Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val Ser Asn Gly Leu Arg Asp  
 85 90 95

Phe Ala Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala  
100 105 110

Ala Gly Glu Ala Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala  
115 120 125

Val Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val Gln Arg  
130 135 140

Arg His Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp  
145 150 155 160

Trp Phe Val Gly Val Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp  
165 170 175

Arg Glu Gln Ala Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp  
180 185 190

Ser Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp  
195 200 205

Thr Val Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser  
210 215 220

Phe Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr  
225 230 235 240

Leu Val Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala Pro  
245 250 255

Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser Val Pro  
260 265 270

Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu  
275 280 285

Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser Arg Thr Arg Tyr  
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Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro Cys Pro Glu Leu Glu  
305 310 315 320

Glu Glu Ala Glu Cys Val Pro Asp Asn Cys Val  
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Ser Ile Thr

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Leu Phe Arg

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<213> Homo sapiens

&lt;400&gt; 11

Asp Ala Gly Thr Asp Ser Gly Phe Thr Phe Ser Ser Pro His Phe Ala  
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Thr Ile Pro Gln Asp Thr Val  
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Val Cys Thr Ala Arg Pro Leu Ala Arg Tyr Ser Ile Thr Phe Thr Gly  
35 40 45

Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr Pro Leu Phe Arg Pro  
50 55 60

Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala Ala His Ser Ser Asp Tyr  
65 70 75 80

Ser Met Trp Arg Lys Asn Glu Tyr Val Ser Asn Gly Leu Arg Asp Phe  
85 90 95

Ala Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala Ala  
100 105 110

Gly Glu Lys Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala Val  
115 120 125

Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val His Pro Arg  
130 135 140

His Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp Trp  
145 150 155 160

Phe Val Gly Ile Asp Ser Leu Asp Leu Cys Glu Gly Gly Arg Trp Lys  
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165

170

175

Glu Gln Val Val Leu Asp Leu Tyr Pro His Asp Ala Gly Thr Asp Ser  
180 185 190

Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr  
195 200 205

Val Thr Glu Ile Thr Ala Ser Ser Pro Ser His Pro Ala Asn Ser Phe  
210 215 220

Tyr Tyr Pro Arg Leu Lys Ser Leu Pro Pro Ile Ala Lys Val Thr Phe  
225 230 235 240

Val Arg Leu Arg Gln Ser Pro Arg Ala Phe Ala Pro Pro Ser Leu Asp  
245 250 255

Leu Ala Ser Arg Gly Asn Glu Ile Val Asp Ser Leu Ser Val Pro Glu  
260 265 270

Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu Cys  
275 280 285

Gly Gly Pro Cys Gly Lys Leu Gly Ala Lys Ser Arg Thr Arg Tyr Val  
290 295 300

Arg Val Gln Pro Ala Asn Asn Gly Thr Pro Cys Pro Glu Leu Glu Glu  
305 310 315 320

Glu Ala Glu Cys Ala Pro Asp Asn Cys Val  
325 330